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<input type="checkbox"/>	L1	gilbert.in. and wakarchuk.in.	39

END OF SEARCH HISTORY

1. [20060166317](#). 11 Dec 03. 27 Jul 06. Nucleic acids encoding sialyltransferases from *C. jejuni*. [Gilbert](#), Michel, et al. 435/69.1; 435/193 435/252.3 435/471 435/72 536/23.2 C07H21/04 20060101 C12N1/21 20060101 C12N15/74 20060101 C12N9/10 20060101 C12P19/00 20060101 C12P21/06 20060101

- ☐ 2. [20050227248](#). 08 Oct 04. 13 Oct 05. Polypeptides having beta-1,4-GalNAc transferase activity. [Gilbert](#), Michel, et al. 435/6; 435/193 435/252.3 435/471 435/69.1 435/85 536/23.2 536/53 C12Q001/68 C07H021/04 C12P019/28 C12N009/10 C12N015/74 C12N001/21.

- ☐ 3. [20050084891](#). 08 Oct 04. 21 Apr 05. Beta 1,4-N-acetylgalactosaminyl transferases from *C. jejuni*. [Gilbert](#), Michel, et al. 435/6; 435/193 435/252.3 435/320.1 435/69.1 514/54 536/23.2 536/53 C12Q001/68 A61K031/739 C07H021/04 C08B037/00 C12N009/10 C12N015/74.

- ☐ 4. [20050064550](#). 22 Apr 04. 24 Mar 05. Nucleic acids encoding beta 1,4-N-acetylgalactosaminyltransferases from *C. Jejuni*. [Gilbert](#), Michel, et al. 435/69.1; 435/193 435/252.33 435/320.1 536/23.2 536/53 C12N009/10 C12N001/21 C12N015/74.

- ☐ 5. [20050048630](#). 08 Oct 04. 03 Mar 05. Nucleic acids encoding beta 1,4-N-acetylgalactosaminyltransferases from *C. jejuni*. [Gilbert](#), Michel, et al. 435/85; 435/193 435/252.3 435/320.1 435/69.1 514/54 536/23.2 536/53 C07H021/04 C08B037/00 A61K031/739 C12P019/28 C12N009/10 C12N015/74.

- ☐ 6. [20040265875](#). 24 Apr 04. 30 Dec 04. Beta 1,4-N-acetylgalactosaminyltransferases form *C. jejuni*. [Gilbert](#), Michel, et al. 435/6; 435/193 435/252.3 435/320.1 435/69.1 536/23.2 536/53 C12Q001/68 C07H021/04 C12N009/10 C08B037/00 C12N015/74.

- ☐ 7. [20040259203](#). 19 May 04. 23 Dec 04. Nucleic acids encoding beta 1,3-galactosyltransferases from *C. jejuni*. [Gilbert](#), Michel, et al. 435/69.1; 435/193 435/252.3 435/320.1 514/54 536/23.2 536/53 C08B037/00 C07H021/04 C12N009/10.

- ☐ 8. [20040259140](#). 21 May 04. 23 Dec 04. Beta 1,3-galactosyltransferases from *C. jejuni*. [Gilbert](#), Michel, et al. 435/6; 435/193 435/252.3 435/320.1 435/69.1 536/23.2 536/53 C12Q001/68 C07H021/04 C12P019/18 C08B037/00 C12N009/10.

- ☐ 9. [20040229313](#). 08 Apr 04. 18 Nov 04. Sialyltransferases from *C. jejuni*. [Gilbert](#), Michel, et al. 435/69.1; 435/193 435/252.33 435/320.1 514/54 536/23.2 536/54 A61K031/739 C07H021/04 C12N009/10 C12N001/21 C12N015/74.

- ☐ 10. [20040229272](#). 17 May 04. 18 Nov 04. Beta 1,3-galactosyltransferases from *C. jejuni*. [Gilbert](#), Michel, et al. 435/6; 435/193 435/252.3 435/320.1 435/69.1 435/89 536/23.2 536/53 C12Q001/68 C07H021/04 C12P019/30 C12N009/10 C12N015/74.

- ☐ 11. [20040229263](#). 08 Apr 04. 18 Nov 04. Los locus from *C.jejuni*. [Gilbert](#), Michel, et al. 435/6; 435/193 435/252.3 435/320.1 435/69.1 435/89 536/23.2 536/53 C12Q001/68 C07H021/04 C12P019/30 C12N009/10 C12N015/74.

- ☐ 12. [20040219638](#). 14 May 04. 04 Nov 04. Nucleic acids encoding beta 1,3-galactosyltransferases from *C.jejuni*. [Gilbert](#), Michel, et al. 435/69.3; 435/193 435/252.3 435/320.1 514/54 536/23.2 536/53 C07H021/04 A61K031/715 C08B037/00 C12N009/10.

- ☐ 13. [20040203113](#). 12 May 04. 14 Oct 04. Nucleic acids encoding beta 1,4-N-

acetylgalactosaminyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/69.1; 435/193 435/320.1 435/325 536/23.2 536/53 C12P019/18 C07H021/04 C12N009/10 C08B037/00.

☐ 14. 20040203112. 12 May 04. 14 Oct 04. Beta1,4-N-acetylgalactosaminyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/69.1; 435/193 435/320.1 435/325 536/23.2 536/53 C12P019/18 C07H021/04 C08B037/00 C12N009/10.

☐ 15. 20040203103. 07 Apr 04. 14 Oct 04. Nucleic acids encoding sialyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/69.1; 435/193 435/252.3 435/320.1 435/325 536/23.2 C12N009/10 C07H021/04 C12N001/21.

☐ 16. 20040180406. 11 Dec 03. 16 Sep 04. Nucleic acids encoding sialyltransferases from *C. jejuni*. Gilbert, Michel, et al. 435/69.1; 435/193 435/200 435/252.3 435/320.1 536/23.2 536/53 C12N009/10 C07H021/04 C08B037/00 C12N001/21 C12N015/74.

☐ 17. 20040152165. 11 Mar 04. 05 Aug 04. Lipopolysaccharide alpha -2,3 sialyltransferase of *Campylobacter jejuni* and its uses. Gilbert, Michel, et al. 435/69.1; 435/193 435/320.1 435/325 536/23.2 536/53 C12N009/10 C07H021/04 C08B037/00.

☐ 18. 20030186414. 11 Dec 02. 02 Oct 03. Nucleic acid that encodes a fusion protein. Gilbert, Michel, et al. 435/193; 435/320.1 435/325 435/6 435/69.1 536/23.2 C12N009/10 C12Q001/68 C07H021/04 C12P021/02 C12N005/06.

☐ 19. 20030180928. 11 Dec 02. 25 Sep 03. Fusion protein comprising a UDP-Galnac 4' epimerase and a galnac transferase. Gilbert, Michel, et al. 435/193; 435/320.1 435/325 435/6 435/69.7 536/23.2 C12N009/10 C12Q001/68 C07H021/04 C12P021/04 C12N005/06.

☐ 20. 20030157658. 21 Nov 02. 21 Aug 03. Polypeptides having beta-1,4-GalNAc transferase activity. Gilbert, Michel, et al. 435/84; 435/193 435/252.33 435/320.1 435/69.1 536/23.2 536/53 C12P021/02 C12N001/21 C07H021/04 C08B037/00 C12P019/26 C12N009/10 C12N015/74.

☐ 21. 20030157657. 21 Nov 02. 21 Aug 03. Polypeptides having beta-1,3-galactosyl transferase activity. Gilbert, Michel, et al. 435/84; 435/193 435/252.3 435/320.1 435/69.1 536/23.2 536/53 C12P019/26 C07H021/04 C08B037/00 C12N009/10 C12P021/02 C12N001/21 C12N015/74.

☐ 22. 20030157656. 21 Nov 02. 21 Aug 03. Nucleic acids encoding beta-1,4-GalNAc transferase. Gilbert, Michel, et al. 435/84; 435/193 435/252.33 435/320.1 435/69.1 536/23.2 536/53 C12P019/26 C08B037/00 C12N009/10 C07H021/04 C12P021/02 C12N001/21 C12N015/74.

☐ 23. 20030157655. 21 Nov 02. 21 Aug 03. Nucleic acids encoding polypeptides with beta-1,3-galactosyl transferase activity. Gilbert, Michel, et al. 435/84; 435/193 435/252.3 435/320.1 435/69.1 536/23.2 536/53 C12P019/26 C12P021/02 C12N001/21 C07H021/04 C08B037/00 C12N009/10 C12N015/74.

☐ 24. 20030148459. 21 Nov 02. 07 Aug 03. Polypeptides having sialyltransferase activity. Gilbert, Michel, et al. 435/69.1; 435/193 435/252.3 435/320.1 536/23.2 536/53 C12P021/02 C12N001/21 C07H021/04 C12N009/10.

☐ 25. 20030049270. 29 Jan 02. 13 Mar 03. Lipopolysaccharide alpha-2,3 sialyltransferase of *Campylobacter jejuni* and its uses. Gilbert, Michel, et al. 424/190.1; 435/193 435/252.3 435/320.1 435/69.1 536/23.2 536/53 A61K039/02 C07H021/04 C12P021/02 C12N001/21 C08B037/00

C12N009/10 C12N015/74.

☐ 26. [20020042369](#). 21 Mar 01. 11 Apr 02. Campylobacter glycosyltransferases for biosynthesis of gangliosides and ganglioside mimics. [Gilbert](#), Michel, et al. 514/12; 435/193 435/320.1 435/325 536/23.2 A61K038/17 C07H021/04 C12N009/10.

☐ 27. [20020034805](#). 14 Dec 98. 21 Mar 02. FUSION PROTEINS FOR USE IN ENZYMATIC SYNTHESIS OF OLIGOSACCHARIDES. [GILBERT](#), MICHEL, et al. 435/193; 435/183 435/200 435/320.1 435/325 536/23.2 C12N009/00.

☐ 28. [7078207](#). 08 Oct 04; 18 Jul 06. Polypeptides having .beta.-1,4-GalNAc transferase activity. [Gilbert](#); Michel, et al. 435/193; 435/252.33 435/69.7 530/412. C07K1/00 20060101 C12N1/20 20060101 C12P21/00 20060101 C12N9/10 20060101 .

☐ 29. [7026147](#). 11 Dec 03; 11 Apr 06. .alpha.-2,3-Sialyltransferase polypeptides. [Gilbert](#); Michel, et al. 435/193; 435/69.7. C12P21/00 20060101 C12N9/10 20060101 .

☐ 30. [6911337](#). 21 Nov 02; 28 Jun 05. Nucleic acids encoding .beta.-1,4-GalNAc transferase. [Gilbert](#); Michel, et al. 435/252.3; 435/193 435/252.33 435/320.1 435/325 536/23.2. C07H021/04 C12N009/10 C12N015/00 C12N001/20 .

☐ 31. [6905867](#). 21 Nov 02; 14 Jun 05. Nucleic acids encoding polypeptides with .beta.1,3-galactosyl transferase activity. [Gilbert](#); Michel, et al. 435/252.3; 435/193 435/252.33 435/254.1 435/320.1 435/325 536/23.2. C12N009/10 C12N001/20 C12N015/00 C12N015/63 C07H021/04 .

☐ 32. [6825019](#). 21 Nov 02; 30 Nov 04. Polypeptides having .beta.-1,3-galactosyl transferase activity. [Gilbert](#); Michel, et al. 435/193; 435/252.3 435/252.33. C12N009/10 C12N001/20 .

☐ 33. [6723545](#). 21 Nov 02; 20 Apr 04. Polypeptides having .beta.-1,4-GalNAc transferase activity. [Gilbert](#); Michel, et al. 435/193; . C12N009/10 .

☐ 34. [6709834](#). 29 Jan 02; 23 Mar 04. Lipopolysaccharide .alpha.-2,3 sialyltransferase of campylobacter jejuni and its uses. [Gilbert](#); Michel, et al. 435/15; 435/183 435/193 435/220 435/252.3 435/320.1 435/4 435/41 435/6 435/7.2 435/85 435/97 530/350. C12Q001/48 .

☐ 35. [6699705](#). 21 Mar 01; 02 Mar 04. Campylobacter glycosyltransferases for biosynthesis of gangliosides and ganglioside mimics. [Gilbert](#); Michel, et al. 435/252.3; 435/193 435/252.33 435/320.1 435/325 536/23.2. C07H021/04 C12N001/20 C12N015/63 C12N009/10 .

☐ 36. [6689604](#). 18 Mar 99; 10 Feb 04. Lipopolysaccharide .alpha.-2,3 sialyltransferase of Campylobacter jejuni and its uses. [Gilbert](#); Michel, et al. 435/320.1; 435/252.3 435/252.33 435/346 435/6 435/68.1 435/69.1 435/69.3 435/70.2 435/71.1 435/71.2 435/74 435/822 514/54 536/23.1 536/23.2 536/24.3. C12N015/00 .

☐ 37. [6503744](#). 31 Jan 00; 07 Jan 03. Campylobacter glycosyltransferases for biosynthesis of gangliosides and ganglioside mimics. [Gilbert](#); Michel, et al. 435/193; 435/183 435/252.3 435/320.1 536/23.2. C12N009/10 C12N009/00 C12N001/20 C12N015/00 .

☐ 38. [6210933](#). 01 Sep 99; 03 Apr 01. Recombinant .alpha.-2,3-sialyltransferases and their uses. [Gilbert](#); Michel, et al. 435/97; 435/193 536/23.2. C12N009/10 C12N015/54 C12D019/18 .

☐ 39. 6096529. 07 Jun 97; 01 Aug 00. Recombinant .alpha.-2,3-sialyltransferases and their uses. Gilbert; Michel, et al. 435/252.3; 435/193 435/252.33 435/320.1 435/325 536/23.2. C12N015/54 C12N001/21 C12N005/10 C12N009/10 .

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(GILBERT.IN. AND WAKARCHUK.IN.).PGPB,USPT.	39

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OM protein - protein search, using sw model

Run on: October 31, 2006, 04:02:56 ; Search time 275.132 Seconds
(without alignments)
714.577 Million cell updates/sec

Title: US-10-799-016A-2
Perfect score: 2267
Sequence: 1 MTRTRMENELIVSKNMQNII.....YIKFIFKDVPRLKREFEKG 430

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2267	100.0	430	2	AAy45221	Aay45221 Campyloba
2	753	33.2	291	3	AAy97210	Aay97210 Campyloba
3	753	33.2	291	6	ABJ18480	Abj18480 Campyloba
4	749	33.0	291	6	ABJ18484	Abj18484 Campyloba
5	748	33.0	291	3	AAy97211	Aay97211 Campyloba
6	748	33.0	291	6	ABJ18481	Abj18481 Campyloba

7	746	32.9	291	3	AA97204	Aay97204	Campyloba
8	746	32.9	291	6	ABJ18479	Abj18479	Campyloba
9	743	32.8	291	3	AA97212	Aay97212	Campyloba
10	743	32.8	291	6	ABJ18482	Abj18482	Campyloba
11	739	32.6	291	6	ABJ18485	Abj18485	Campyloba
12	680.5	30.0	294	3	AA97215	Aay97215	Campyloba
13	680.5	30.0	294	6	ABJ18483	Abj18483	Campyloba
14	553	24.4	303	6	ABR40195	Abr40195	alpha-2,3
15	204.5	9.0	612	9	ADY30892	Ady30892	Campyloba
16	204.5	9.0	625	9	ADY30893	Ady30893	Campyloba
17	204.5	9.0	625	9	AED82948	Aed82948	Hyperimmu
18	172	7.6	622	6	ABU39169	Abu39169	Protein e
19	172	7.6	622	7	ADF29255	Adf29255	Bacterial
20	172	7.6	622	7	ADG32464	Adg32464	Pasteurel
21	162	7.1	562	8	ADT61991	Adt61991	Escherich
22	162	7.1	563	6	ABP58097	Abp58097	Escherich
23	143.5	6.3	1351	3	AAB18290	Aab18290	Plasmodiu
24	143	6.3	1283	8	ADP74638	Adp74638	Amino aci
25	141	6.2	367	3	AAB05956	Aab05956	Protein d
26	139.5	6.2	726	5	ABB77613	Abb77613	AmEPV NTP
27	139	6.1	476	3	AA54039	Aay54039	Amino aci
28	139	6.1	476	5	ABG92539	Abg92539	Platelet
29	139	6.1	476	7	ADG34449	Adg34449	Platelet
30	139	6.1	503	2	AAR22667	Aar22667	50 kD sub
31	138.5	6.1	2295	3	AAB18180	Aab18180	Plasmodiu
32	138	6.1	471	2	AA20061	Aay20061	B. burgdo
33	138	6.1	490	2	AA20060	Aay20060	B. burgdo
34	138	6.1	490	6	ABU19083	Abu19083	Protein e
35	137.5	6.1	611	5	ABB09492	Abb09492	AmEPV sec
36	137	6.0	471	3	AA54040	Aay54040	Amino aci
37	136	6.0	1123	3	AA58277	Aay58277	Heliothis
38	136	6.0	1817	3	AAB18301	Aab18301	Plasmodiu
39	136	6.0	2485	3	AAB18172	Aab18172	Plasmodiu
40	134	5.9	1021	2	AAW98555	Aaw98555	H. pylori
41	133	5.9	581	6	ABM73091	Abm73091	Staphyloc
42	132.5	5.8	863	6	ADB08930	Adb08930	Alloiococ
43	132	5.8	971	8	ADM57326	Adm57326	Recombina
44	132	5.8	2013	3	AAB18265	Aab18265	Plasmodiu
45	132	5.8	2133	8	ADP25432	Adp25432	Plasmodiu

ALIGNMENTS

RESULT 1

AA45221

ID AA45221 standard; protein; 430 AA.

XX

AC AA45221;

XX

DT 05-JAN-2000 (first entry)

XX

DE Campylobacter jejuni alpha-2,3-sialyltransferase protein.

XX

KW Campylobacter jejuni; alpha-2,3-sialyltransferase; cst-I; acceptor;
KW lipopolysaccharide; galactose residue; sialic acid molecule.

XX

OS Campylobacter jejuni.

XX

PN WO9949051-A1.

XX

PD 30-SEP-1999.
 XX
 PF 22-MAR-1999; 99WO-CA000238.
 XX
 PR 20-MAR-1998; 98US-0078891P.
 PR 18-MAR-1999; 99US-00272960.
 XX
 PA (CANA) NAT RES COUNCIL CANADA.
 XX
 PI Gilbert M, Wakarchuk WW;
 XX
 DR WPI; 1999-601216/51.
 DR N-PSDB; AAZ25693.
 XX
 PT New sialyltransferases useful for adding sialyl residues to acceptor
 PT molecules.
 XX
 PS Claim 27; Fig 2; 47pp; English.
 XX
 CC The present sequence represents *Campylobacter jejuni* alpha-2,3-
 CC sialyltransferase which is encoded by the *cst-I* gene. The alpha-2,3-
 CC sialyltransferase protein is useful for producing desired carbohydrate
 CC structures by contacting the acceptor molecule (which has a terminal
 CC galactose residue) with an activated sialic acid molecule. The terminal
 CC galactose residue is linked to a second residue (Glc or a GlcNac, or
 CC GlcNac or GalNac) in the acceptor molecule through a beta-1,3 or beta-1,4
 CC linkage, respectively. The activated sialic acid is CMP-Neu5Ac. The
 CC polynucleotides and polypeptides facilitate the improved production of
 CC desired structures and nucleic acids encoding sialyltransferases
 XX
 SQ Sequence 430 AA;

Query Match 100.0%; Score 2267; DB 2; Length 430;
 Best Local Similarity 100.0%; Pred. No. 1.2e-195;
 Matches 430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTRTRMENELIVSKNMQNI	IIAGNGPSLKNIN	YKRLPREYDV	FRCNQFYFEDKYYLGKKI	60
Db	1	MTRTRMENELIVSKNMQNI	IIAGNGPSLKNIN	YKRLPREYDV	FRCNQFYFEDKYYLGKKI	60
Qy	61	KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLG				120
Db	61	KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLG				120
Qy	121	YEVIENTLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFE				180
Db	121	YEVIENTLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFE				180
Qy	181	AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSIN				240
Db	181	AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSIN				240
Qy	241	INNFTLENKHNNNSINDILLTDNTPGVSYKNQLKADNKIMLNFYNILHSKDNLIKFLNK				300
Db	241	INNFTLENKHNNNSINDILLTDNTPGVSYKNQLKADNKIMLNFYNILHSKDNLIKFLNK				300
Qy	301	EIAVLKKQTQRAKARIQNHLSYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAY				360
Db	301	EIAVLKKQTQRAKARIQNHLSYKLGQALIINSKSVLGFLSLPFIILSIVISHKQEQKAY				360
Qy	361	KFKVKKNPNLALPPLETYPDYNEALKEKECFYKLGEEFIKAGKNWYGEgyIKFIFKDVP				420

Db	361	 KFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGEEFIKAGKNWYGEGYIKFIFKDVP	420
Qy	421	RLKREFEKGE	430
Db	421	 RLKREFEKGE	430

SCORE Search Results Details for Application 10799016 and Search Result us-10-799-016a-2.rup.

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OM protein - protein search, using sw model

```
Run on:      October 31, 2006, 04:07:56 ; Search time 217.269 Seconds
              (without alignments)
              1830.710 Million cell updates/sec
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Title:          US-10-799-016A-2
Perfect score: 2267
Sequence:      1 MTRTRMENELIVSKNMQNI.....YIKFIFKDVPRLKREFEKGE 430
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

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Database :      UniProt_7.2:*
1:  uniprot_sprot:*
2:  uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2267	100.0	430	2	Q9RGF1_CAMJE	Q9rgf1 campylobact
2	2261	99.7	430	2	Q32VR8_CAMJE	Q32vr8 campylobact
3	775.5	34.2	292	2	Q5DT12_CAMJE	Q5dt12 campylobact
4	750	33.1	291	2	Q93MQ0_CAMJE	Q93mq0 campylobact

5	749	33.0	291	2	Q9F0M9_CAMJE	Q9f0m9	campylobact
6	746	32.9	291	2	Q9LAK3_CAMJE	Q9lak3	campylobact
7	745	32.9	291	2	Q938X6_CAMJE	Q938x6	campylobact
8	745	32.9	291	2	Q93CZ5_CAMJE	Q93cz5	campylobact
9	743	32.8	284	2	Q50FZ0_CAMJE	Q50fz0	campylobact
10	743	32.8	291	2	Q9L9Q5_CAMJE	Q9l9q5	campylobact
11	739	32.6	263	2	Q2TKA8_CAMJE	Q2tka8	campylobact
12	739	32.6	291	2	Q93D05_CAMJE	Q93d05	campylobact
13	680.5	30.0	294	2	Q7BP25_CAMJE	Q7bp25	campylobact
14	626.5	27.6	534	2	Q32VQ2_CAMJE	Q32vq2	campylobact
15	601.5	26.5	576	2	Q32VR2_CAMJE	Q32vr2	campylobact
16	601.5	26.5	576	2	Q5W602_CAMJE	Q5w602	campylobact
17	590	26.0	569	2	Q5M6Q2_CAMJE	Q5m6q2	campylobact
18	587.5	25.9	326	2	Q4QM36_HAEI8	Q4qm36	haemophilus
19	583	25.7	569	2	Q6EF79_CAMJE	Q6ef79	campylobact
20	577	25.5	505	2	Q32VQ8_CAMJE	Q32vq8	campylobact
21	572	25.2	569	2	Q6EF56_CAMJE	Q6ef56	campylobact
22	571	25.2	391	2	Q5W603_CAMJE	Q5w603	campylobact
23	556	24.5	501	2	Q32VQ3_CAMJE	Q32vq3	campylobact
24	553	24.4	303	2	Q9CLP3_PASMU	Q9clp3	pasteurella
25	550	24.3	320	2	Q4QNI8_HAEI8	Q4qni8	haemophilus
26	546	24.1	400	2	Q32VR3_CAMJE	Q32vr3	campylobact
27	473.5	20.9	650	2	Q5HT01_CAMJR	Q5ht01	campylobact
28	453	20.0	582	2	Q5M6U5_CAMJE	Q5m6u5	campylobact
29	412.5	18.2	365	2	Q4HEL4_CAMCO	Q4hel4	campylobact
30	408	18.0	462	2	Q4HEJ9_CAMCO	Q4hej9	campylobact
31	405.5	17.9	130	2	Q6EBB5_CAMJE	Q6ebb5	campylobact
32	392.5	17.3	177	2	Q4HEK5_CAMCO	Q4hek5	campylobact
33	359	15.8	502	2	Q5M6M5_CAMJE	Q5m6m5	campylobact
34	354	15.6	832	2	Q5M6M2_CAMJE	Q5m6m2	campylobact
35	340	15.0	639	2	Q5HT02_CAMJR	Q5ht02	campylobact
36	339	15.0	231	1	Y352_HAEIN	P24324	haemophilus
37	311	13.7	374	2	Q4HR89_CAMUP	Q4hr89	campylobact
38	301.5	13.3	582	2	Q9PMM6_CAMJE	Q9pmm6	campylobact
39	297.5	13.1	407	2	Q4HEL1_CAMCO	Q4hel1	campylobact
40	284.5	12.5	560	2	Q4HR98_CAMUP	Q4hr98	campylobact
41	276.5	12.2	502	2	Q4HLH9_CAMLA	Q4hlh9	campylobact
42	268	11.8	566	2	Q6EF57_CAMJE	Q6ef57	campylobact
43	267.5	11.8	459	2	Q5M6S8_CAMJE	Q5m6s8	campylobact
44	263.5	11.6	401	2	Q4HKU2_CAMLA	Q4hku2	campylobact
45	260	11.5	448	2	Q4HR95_CAMUP	Q4hr95	campylobact

ALIGNMENTS

RESULT 1

Q9RGF1_CAMJE

ID Q9RGF1_CAMJE PRELIMINARY; PRT; 430 AA.

AC Q9RGF1;

DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.

DT 01-MAY-2000, sequence version 1.

DT 07-FEB-2006, entry version 16.

DE Alpha-2,3-sialyltransferase.

GN Name=cst-I;

OS Campylobacter jejuni.

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;

OC Campylobacteraceae; Campylobacter.

OX NCBI_TaxID=197;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=OH4384;
 RX MEDLINE=20127862; PubMed=10660542; DOI=10.1074/jbc.275.6.3896;
 RA Gilbert M., Brisson J.-R., Karwaski M.-F., Michniewicz J.,
 RA Cunningham A.-M., Wu Y., Young N.M., Wakarchuk W.W.;
 RT "Biosynthesis of ganglioside mimics in *Campylobacter jejuni* OH4384.
 RT Identification of the glycosyltransferase genes, enzymatic synthesis
 RT of model compounds, and characterization of nanomole amounts by 600-
 RT MHz (1)H and (13)C NMR analysis.";
 RL J. Biol. Chem. 275:3896-3906(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=OH4384;
 RA Gilbert M., Wakarchuk W.W.;
 RT "Lipopolysaccharide .alpha.-2,3 sialyltransferase of *campylobacter*.";
 RL Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
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 CC -----
 DR EMBL; AF130466; AAF13495.1; -; Genomic_DNA.
 DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
 DR InterPro; IPR009251; CST-I.
 DR Pfam; PF06002; CST-I; 1.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 430 AA; 50396 MW; 1D03B6797169425C CRC64;

Query Match 100.0%; Score 2267; DB 2; Length 430;
 Best Local Similarity 100.0%; Pred. No. 5.5e-137;
 Matches 430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTRTRMENELIVSKNMQNI	IIAGNGPSLKNIN	YKRLPREYDVFR	CNQFYFEDKY	YLGKKI	60
Db	1	MTRTRMENELIVSKNMQNI	IIAGNGPSLKNIN	YKRLPREYDVFR	CNQFYFEDKY	YLGKKI	60
Qy	61	KAVFFNP	GVFLQQYHTAKQLIL	KNEYEIKNIFCSTF	NLPFIESNDFLHQFY	NFFPDAKLG	120
Db	61	KAVFFNP	GVFLQQYHTAKQLIL	KNEYEIKNIFCSTF	NLPFIESNDFLHQFY	NFFPDAKLG	120
Qy	121	YEV	IENLKEFYAYIKYNEI	YFNKRITSGVYMCAIA	IALGYKTIYLCGIDFY	EGDVIYPFE	180
Db	121	YEV	IENLKEFYAYIKYNEI	YFNKRITSGVYMCAIA	IALGYKTIYLCGIDFY	EGDVIYPFE	180
Qy	181	AMSTNIKTIFPGIKDFKPS	NCHSKEYDIEALKLLKSI	YKVNIYALCDDSILAN	HFP	PLSIN	240
Db	181	AMSTNIKTIFPGIKDFKPS	NCHSKEYDIEALKLLKSI	YKVNIYALCDDSILAN	HFP	PLSIN	240
Qy	241	INN	NFTLENKHNN	SINDILLTDNTPGV	SFYKNQLKADNKIM	LN	300
Db	241	INN	NFTLENKHNN	SINDILLTDNTPGV	SFYKNQLKADNKIM	LN	300
Qy	301	EIAVLKKQTTQRAKARIQ	NHLSYKLGQALIINSK	SVLGFLSLPFIILSIV	ISHKQEQKAY	360	
Db	301	EIAVLKKQTTQRAKARIQ	NHLSYKLGQALIINSK	SVLGFLSLPFIILSIV	ISHKQEQKAY	360	
Qy	361	KFKVKKNPNLALPPLETYP	PDYNEALKEKECFTYK	LGEEFIKAGKNWYGE	GYIKFIFKDVP	420	
Db	361	KFKVKKNPNLALPPLETYP	PDYNEALKEKECFTYK	LGEEFIKAGKNWYGE	GYIKFIFKDVP	420	
Qy	421	RLKREFEKGE	430				
Db	421	RLKREFEKGE	430				

RESULT 2

Q32VR8_CAMJE

ID Q32VR8_CAMJE PRELIMINARY; PRT; 430 AA.

AC Q32VR8;

DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.

DT 06-DEC-2005, sequence version 1.

DT 07-FEB-2006, entry version 3.

DE Alpha-2,3-sialyltransferase.

GN Name=cstI;

OS Campylobacter jejuni subsp. jejuni.

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;

OC Campylobacteraceae; Campylobacter.

OX NCBI_TaxID=32022;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 43446;

RA Gilbert M., Brochu D., Karwaski M.-F.;

RT "Sequencing of the Cst-I locus of Campylobacter jejuni ATCC 43446.";

RL Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.

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DR EMBL; AY791515; AAX33819.1; -; Genomic_DNA.

DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.

KW Glycosyltransferase; Transferase.

SQ SEQUENCE 430 AA; 50383 MW; 876F9E0583694240 CRC64;

Query Match 99.7%; Score 2261; DB 2; Length 430;

Best Local Similarity 99.8%; Pred. No. 1.3e-136;

Matches 429; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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      |||
Db      1 MTRTRMENELIVSKNMQNI IAGNGPSLKNINYKRLPREYDVFR CNQFYFEDKYYLGKKI 60

Qy     61 KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLG 120
      |||
Db     61 KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLG 120

Qy    121 YEVIENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFE 180
      |||
Db    121 YEVIENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFE 180

Qy    181 AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSIN 240
      |||
Db    181 AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSIN 240

Qy    241 INNNFTLENKHNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNI LHSKDNLIKFLNK 300
      |||
Db    241 INNNFTLENKHNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNI LHSKDTLIKFLNK 300

Qy    301 EIAVLKKQTTQRAKARIQNHL SYKLGQALI INSKSVLGFLSLPFIILSIVISHKQEQKAY 360
      |||
Db    301 EIAVLKKQTTQRAKARIQNHL SYKLGQALI INSKSVLGFLSLPFIILSIVISHKQEQKAY 360

Qy    361 KFKVKKNPNLALPPLETYPDYNEALKEKECF TYKLGE EFIKAGKNWYGEGYIKFIFKDVP 420
      |||
Db    361 KFKVKKNPNLALPPLETYPDYNEALKEKECF TYKLGE EFIKAGKNWYGEGYIKFIFKDVP 420

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Qy	421	RLKREFEKGE	430
Db	421	RLKREFEKGE	430

SCORE Search Results Details for Application 10799016 and Search Result us-10-799-016a-2_copy_1_328.rup.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10799016 and Search Result us-10-799-016a-2_copy_1_328.rup.

start

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GenCore version 5.1.9
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OM protein - protein search, using sw model

```
Run on:      October 31, 2006, 04:07:56 ; Search time 165.731 Seconds
              (without alignments)
              1830.710 Million cell updates/sec
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Title: US-10-799-016A-2_COPY_1_328
Perfect score: 1732
Sequence: 1 MTRTRMENELIVSKNMQNI.....TTQRAKARIQNHLSYKLGQA 328

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

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Database :      UniProt_7.2:*
           1:  uniprot_sprot:*
           2:  uniprot_trembl:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1732	100.0	430	2	Q9RGF1_CAMJE	Q9rgf1 campylobact
2	1726	99.7	430	2	Q32VR8_CAMJE	Q32vr8 campylobact
3	775.5	44.8	292	2	Q5DT12_CAMJE	Q5dt12 campylobact
4	750	43.3	291	2	Q93MQ0_CAMJE	Q93mq0 campylobact

5	749	43.2	291	2	Q9F0M9_CAMJE	Q9f0m9	campylobact
6	746	43.1	291	2	Q9LAK3_CAMJE	Q9lak3	campylobact
7	745	43.0	291	2	Q938X6_CAMJE	Q938x6	campylobact
8	745	43.0	291	2	Q93CZ5_CAMJE	Q93cz5	campylobact
9	743	42.9	284	2	Q50FZ0_CAMJE	Q50fz0	campylobact
10	743	42.9	291	2	Q9L9Q5_CAMJE	Q9l9q5	campylobact
11	739	42.7	263	2	Q2TKA8_CAMJE	Q2tka8	campylobact
12	739	42.7	291	2	Q93D05_CAMJE	Q93d05	campylobact
13	680.5	39.3	294	2	Q7BP25_CAMJE	Q7bp25	campylobact
14	580	33.5	326	2	Q4QM36_HAEI8	Q4qm36	haemophilus
15	553	31.9	303	2	Q9CLP3_PASMU	Q9clp3	pasteurella
16	550	31.8	320	2	Q4QNI8_HAEI8	Q4qni8	haemophilus
17	339	19.6	231	1	Y352_HAEIN	P24324	haemophilus
18	164.5	9.5	576	2	Q32VR2_CAMJE	Q32vr2	campylobact
19	164.5	9.5	576	2	Q5W602_CAMJE	Q5w602	campylobact
20	160.5	9.3	1395	2	Q4Y918_PLACH	Q4y918	plasmodium
21	157	9.1	505	2	Q32VQ8_CAMJE	Q32vq8	campylobact
22	151.5	8.7	502	2	Q4HLH9_CAMLA	Q4hlh9	campylobact
23	151	8.7	44	2	Q4HGT1_CAMCO	Q4hgt1	campylobact
24	150	8.7	692	2	Q30SL2_THIDN	Q30sl2	thiomicrosp
25	149.5	8.6	954	2	Q8IBW2_PLAF7	Q8ibw2	plasmodium
26	149	8.6	960	2	Q25802_PLAFA	Q25802	plasmodium
27	149	8.6	1321	2	Q8IAR1_PLAF7	Q8iar1	plasmodium
28	148.5	8.6	995	2	Q6LFH7_PLAF7	Q6lfh7	plasmodium
29	148.5	8.6	10061	2	Q8I3Z1_PLAF7	Q8i3z1	plasmodium
30	148	8.5	391	2	Q5W603_CAMJE	Q5w603	campylobact
31	148	8.5	400	2	Q32VR3_CAMJE	Q32vr3	campylobact
32	148	8.5	714	2	Q98RL8_GUIITH	Q98rl8	guillardia
33	147.5	8.5	883	2	Q7RD16_PLAYO	Q7rd16	plasmodium
34	147	8.5	1156	2	Q8I474_PLAF7	Q8i474	plasmodium
35	146.5	8.5	803	2	Q4YST0_PLABE	Q4yst0	plasmodium
36	145.5	8.4	569	2	Q5M6Q2_CAMJE	Q5m6q2	campylobact
37	144.5	8.3	569	2	Q6EF56_CAMJE	Q6ef56	campylobact
38	144.5	8.3	2070	2	Q8IJ79_PLAF7	Q8ij79	plasmodium
39	144	8.3	496	2	Q4YHT9_PLABE	Q4yht9	plasmodium
40	144	8.3	522	2	Q4YWZ1_PLABE	Q4y wz1	plasmodium
41	143	8.3	1410	2	Q97230_PLAF7	Q97230	plasmodium
42	143	8.3	5779	2	Q8IBS0_PLAF7	Q8ibs0	plasmodium
43	142.5	8.2	826	2	Q4YP78_PLABE	Q4yp78	plasmodium
44	142	8.2	1739	2	Q8IIJ5_PLAF7	Q8ii j5	plasmodium
45	142	8.2	2723	2	Q8I5X3_PLAF7	Q8i5x3	plasmodium

ALIGNMENTS

RESULT 1

Q9RGF1_CAMJE

ID Q9RGF1_CAMJE PRELIMINARY; PRT; 430 AA.

AC Q9RGF1;

DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.

DT 01-MAY-2000, sequence version 1.

DT 07-FEB-2006, entry version 16.

DE Alpha-2,3-sialyltransferase.

GN Name=cst-I;

OS Campylobacter jejuni.

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;

OC Campylobacteraceae; Campylobacter.

OX NCBI_TaxID=197;

RN [1]

RP NUCLEOTIDE SEQUENCE.

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RC      STRAIN=OH4384;
RX      MEDLINE=20127862; PubMed=10660542; DOI=10.1074/jbc.275.6.3896;
RA      Gilbert M., Brisson J.-R., Karwaski M.-F., Michniewicz J.,
RA      Cunningham A.-M., Wu Y., Young N.M., Wakarchuk W.W.;
RT      "Biosynthesis of ganglioside mimics in Campylobacter jejuni OH4384.
RT      Identification of the glycosyltransferase genes, enzymatic synthesis
RT      of model compounds, and characterization of nanomole amounts by 600-
RT      MHz (1)H and (13)C NMR analysis.";
RL      J. Biol. Chem. 275:3896-3906(2000).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=OH4384;
RA      Gilbert M., Wakarchuk W.W.;
RT      "Lipopolysaccharide .alpha.-2,3 sialyltransferase of campylobacter.";
RL      Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
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CC      -----
DR      EMBL; AF130466; AAF13495.1; -; Genomic_DNA.
DR      GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR      InterPro; IPR009251; CST-I.
DR      Pfam; PF06002; CST-I; 1.
KW      Glycosyltransferase; Transferase.
SO      SEQUENCE      430 AA;  50396 MW;  1D03B6797169425C CRC64;

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Query Match 100.0%; Score 1732; DB 2; Length 430;
Best Local Similarity 100.0%; Pred. No. 5.2e-110;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MTRTRMENELIVSKNMQNI I IAGNGPSLKNIN YKRLPREYDVFRCNQFYFEDKY YLGKKI	60
Qy	61	KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNL PFIESNDFLHQFYNFFPDAKLG	120
Db	61	KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNL PFIESNDFLHQFYNFFPDAKLG	120
Qy	121	YEV IENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFE	180
Db	121	YEV IENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFE	180
Qy	181	AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSIN	240
Db	181	AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSIN	240
Qy	241	INNNFTLENKHNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNI LHSKDNLIKFLNK	300
Db	241	INNNFTLENKHNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNI LHSKDNLIKFLNK	300
Qy	301	EIAVLKKQTTQRAKARIQNHL SYKLGQA	328
Db	301	EIAVLKKQTTQRAKARIQNHL SYKLGQA	328

RESULT 2

Q32VR8_CAMJE
ID Q32VR8_CAMJE PRELIMINARY; PRT; 430 AA.
AC Q32VR8;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.

DT 07-FEB-2006, entry version 3.
 DE Alpha-2,3-sialyltransferase.
 GN Name=cstI;
 OS Campylobacter jejuni subsp. jejuni.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Campylobacteraceae; Campylobacter.
 OX NCBI_TaxID=32022;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 43446;
 RA Gilbert M., Brochu D., Karwaski M.-F.;
 RT "Sequencing of the Cst-I locus of Campylobacter jejuni ATCC 43446."
 RL Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
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 DR EMBL; AY791515; AAX33819.1; -; Genomic_DNA.
 DR GO; GO:0016757; F:transférase activity, transferring glycosyl. . .; IEA.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 430 AA; 50383 MW; 876F9E0583694240 CRC64;

Query Match 99.7%; Score 1726; DB 2; Length 430;
 Best Local Similarity 99.7%; Pred. No. 1.3e-109;
 Matches 327; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MTRTRMENELIVSKNMQNI	IIIAGNGPSLKNIN	YKRLPREYDVFR	CNQFYFEDKYYLGKKI	60
Db	1	MTRTRMENELIVSKNMQNI	IIIAGNGPSLKNIN	YKRLPREYDVFR	CNQFYFEDKYYLGKKI	60
Qy	61	KAVFFNPGVFLQQYHTAK	QLILKNEYEIKNIFC	STFNLPIESNDFLHQ	FYNFFPDAKLG	120
Db	61	KAVFFNPGVFLQQYHTAK	QLILKNEYEIKNIFC	STFNLPIESNDFLHQ	FYNFFPDAKLG	120
Qy	121	YEVIENTLKEFYAYIKYNE	IYFNKRITSGVYMCA	IAIALGYKTIYLCG	IDFYEGDVIYPFE	180
Db	121	YEVIENTLKEFYAYIKYNE	IYFNKRITSGVYMCA	IAIALGYKTIYLCG	IDFYEGDVIYPFE	180
Qy	181	AMSTNIKTIFPGIKDFKPS	NCHSKEYDIEALKLL	KSIYKVNIYALCDD	SILANHFPLSIN	240
Db	181	AMSTNIKTIFPGIKDFKPS	NCHSKEYDIEALKLL	KSIYKVNIYALCDD	SILANHFPLSIN	240
Qy	241	INNFTLENKHNN	SINDILLTDNTPGV	SFYKNQLKADNKIM	LNLFYNIH	SKDNLIKFLNK 300
Db	241	INNFTLENKHNN	SINDILLTDNTPGV	SFYKNQLKADNKIM	LNLFYNIH	SKDTLIKFLNK 300
Qy	301	EIAVLKKQTTQRAKARIQ	NHLSYKLGQA			328
Db	301	EIAVLKKQTTQRAKARIQ	NHLSYKLGQA			328

RESULT 3

Q5DT12_CAMJE

ID Q5DT12_CAMJE PRELIMINARY; PRT; 292 AA.

AC Q5DT12;

DT 29-MAR-2005, integrated into UniProtKB/TrEMBL.

DT 29-MAR-2005, sequence version 1.

DT 07-FEB-2006, entry version 4.

DE Putative alpha-2,3/-2,8 sialyltransferase.

OS Campylobacter jejuni.

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;

OC Campylobacteraceae; Campylobacter.
 OX NCBI_TaxID=197;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MF6;
 RA Gilbert M., Karwaski M.-F., Godschalk P.C.R., Brochu D., Endtz H.P.,
 RA Cunningham A.;
 RT "Sequencing of the lipooligosaccharide biosynthesis locus of
 RT Campylobacter jejuni MF6.";
 RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
 CC -----
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 CC -----
 DR EMBL; AY422196; AAR82857.1; -; Genomic_DNA.
 DR SMR; Q5DT12; 1-259.
 DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
 DR InterPro; IPR009251; CST-I.
 DR Pfam; PF06002; CST-I; 1.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 292 AA; 34658 MW; 1AAFD7B6FF7B0A2F CRC64;

Query Match 44.8%; Score 775.5; DB 2; Length 292;
 Best Local Similarity 53.6%; Pred. No. 6.6e-45;
 Matches 147; Conservative 42; Mismatches 78; Indels 7; Gaps 2;

Qy 16 MQNIIIAGNGPSLKNINYKRLPREYDVFRNCQFYFEDKYYLGKKIKAVFFNPGVFLQQYH 75
 | : :| | | | | | | | | | | :| | | :| | | | | | | | | | | | | | | | :| :| :| :|
 Db 1 MKKVIIAGNGPSLKEIDYSRLPNDFDVFRNCQFYFEDKYYLGKKCKAVFYNPSLFFEQYY 60

 Qy 76 TAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFPPDAKLGYEVIENTLKEFYAYIK 135
 | | | | | | | | | : | | | | | | | | | :| | | | | | | | | : | | | | | | | |
 Db 61 TLKHLIQNQEYETELIVCSNFNLTHIESENFLKNFYDYFPDAHLGYDFFKQLKEFNAYFK 120

 Qy 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFPGIKD 195
 : :| | | | | :| | | | :| | | | | | | | | | | | | | : | | : | : : : :
 Db 121 FHEIYFNQRITSGIYMCABAIALGYKEIYLSGIDFYQNGSSYAFDTKQKNLLKL---VSN 177

 Qy 196 FKPSNC----HSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENKH 251
 | | | | | | | | | | :| | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 178 FKNDNSHYIGHSKNTDLKALEFLEKTYKIKLYCLCPNSLLANFIELAPNLNSNFIKKKK 237

 Qy 252 NNSINDILLTDNTPGVSFYKNQLKADNKIMLNFY 285
 | | | | : : | | : | | | | |
 Db 238 NNYTKDILIPSSEAYGKFSKNIIFFKKIKIKENIY 271

[Generate Collection](#)[Print](#)**Search Results - Record(s) 1 through 14 of 14 returned.**

-
- ☐ 1. [20060088906](#). 15 Jul 05. 27 Apr 06. Erythropoietin: remodeling and glycoconjugation of erythropoietin. DeFrees; Shawn, et al. 435/68.1; 530/395 C07K14/505 20060101 C12P21/06 20060101
-
- ☐ 2. [20060030521](#). 15 Jul 05. 09 Feb 06. Remodeling and glycoconjugation of peptides. DeFrees; Shawn, et al. 514/8; 424/78.37 435/68.1 525/54.1 530/322 A61K38/14 20060101 A61K38/16 20060101 C12P21/06 20060101
-
- ☐ 3. [20050106658](#). 09 Apr 04. 19 May 05. Remodeling and glycoconjugation of peptides. DeFrees, Shawn, et al. 435/68.1; 530/395 C12P021/06 C07K014/47.
-
- ☐ 4. [20050100982](#). 09 Apr 03. 12 May 05. Factor IX: remodeling and glycoconjugation of factor IX. DeFrees, Shawn, et al. 435/68.1; 530/384 C12P021/06 C07K014/745.
-
- ☐ 5. [20050031584](#). 09 Apr 03. 10 Feb 05. Interleukin-2:remodeling and glycoconjugation of interleukin-2. DeFrees, Shawn, et al. 424/85.2; 530/351 A61K038/20 C07K014/54.
-
- ☐ 6. [20040156837](#). 12 Feb 03. 12 Aug 04. Haemophilus influenzae sialyltransferase and methods of use thereof. Apicella, Michael A., et al. 424/94.5; 435/193 435/320.1 435/325 435/69.1 435/89 536/23.2 536/53 A61K038/48 C12Q001/68 C07H021/04 C08B037/00 C12P019/30.
-
- ☐ 7. [20040142856](#). 09 Apr 03. 22 Jul 04. Glycoconjugation methods and proteins/peptides produced by the methods. DeFrees, Shawn, et al. 514/8; 435/68.1 A61K038/16 C12P021/06.
-
- ☐ 8. [20040137557](#). 05 Nov 02. 15 Jul 04. Remodeling and glycoconjugation of peptides. DeFrees, Shawn, et al. 435/68.1; 530/322 A61K038/16 C12P021/06 C07K009/00.
-
- ☐ 9. [20040132640](#). 09 Apr 03. 08 Jul 04. Glycopegylation methods and proteins/peptides produced by the methods. DeFrees, Shawn, et al. 514/8; 530/395 A61K038/16 C07K014/00 C07K001/113.
-
- ☐ 10. [20040126838](#). 09 Apr 03. 01 Jul 04. Follicle stimulating hormone: remodeling and glycoconjugation of FSH. DeFrees, Shawn, et al. 435/68.1; 530/397 C12Q001/68 C12P021/06.
-
- ☐ 11. [20040115168](#). 09 Apr 03. 17 Jun 04. Interferon beta: remodeling and glycoconjugation of interferon beta. DeFrees, Shawn, et al. 424/85.6; 435/68.1 530/351 C12P021/06 A61K038/21.
-
- ☐ 12. [20040082026](#). 09 Apr 03. 29 Apr 04. Interferon alpha: remodeling and glycoconjugation of interferon alpha. DeFrees, Shawn, et al. 435/68.1; 530/351 C12P021/06 C07K014/54.
-
- ☐ 13. [20040077836](#). 09 Apr 03. 22 Apr 04. Granulocyte colony stimulating factor: remodeling and glycoconjugation of G-CSF. DeFrees, Shawn, et al. 530/351; 435/68.1 C12P021/06 C07K014/535.
-
- ☐ 14. [20040043446](#). 09 Apr 03. 04 Mar 04. Alpha galactosidase a: remodeling and glycoconjugation of alpha galactosidase A. DeFrees, Shawn, et al. 435/68.1; 435/193 435/208 C12P021/06 C12N009/40 C12N009/10.
-

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Term	Documents
GILBERT	63533
GILBERTS	366
(5 NOT (GILBERT.IN.)).PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD.	14
(L5 NOT GILBERT.IN.)).PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD.	14

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WEST Search History

DATE: Wednesday, November 01, 2006

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
	<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR</i>		
<input type="checkbox"/>	L1	\$sialyl-transferase.ti,ab,clm. or \$sialyltransferase.ti,ab,clm.	312
<input type="checkbox"/>	L2	L1 and sialic	210
<input type="checkbox"/>	L3	L2 and campylo\$	62
<input type="checkbox"/>	L4	L3 amd cst\$2	51951
<input type="checkbox"/>	L5	L3 and cst\$2	48
<input type="checkbox"/>	L6	L5 not gilbert.in.	14
<input type="checkbox"/>	L7	(6503744 or 6096529 or 6210933).pn.	5
	<i>DB=EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>		
<input type="checkbox"/>	L8	9949051	3
	<i>DB=PGPB; PLUR=YES; OP=OR</i>		
<input type="checkbox"/>	L9	20022042369	0
<input type="checkbox"/>	L10	200202042369	0
<input type="checkbox"/>	L11	2002042369	0
<input type="checkbox"/>	L12	20022042369	0
<input type="checkbox"/>	L13	200242369	0
<input type="checkbox"/>	L14	20020042369	1
<input type="checkbox"/>	L15	campylobacter same cst\$2	45
<input type="checkbox"/>	L16	L15 not gilbert.in.	21

END OF SEARCH HISTORY

server developed at SIB and the NCBI
BLAST 2 software.

In case of problems, please read the online BLAST help.
If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller
Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein
database search programs. Nucleic Acids Res. 25:3389-3402(1997).

=====

Query: 430 AA
Date run: 2006-11-01 17:47:19 UTC+0100 on blast01.vital-it.ch
Program: NCBI BLASTP 2.2.13 [Nov-27-2005]
Database: UniProtKB
3,570,889 sequences; 1,172,111,231 total letters
UniProt Knowledgebase Release 9 consists of:
UniProtKB/Swiss-Prot Release 51.0 of 31-Oct-2006: 241242 entries
UniProtKB/TrEMBL Release 34.0 of 31-Oct-2006: 3313264 entries

Taxonomic view	NiceBlast view	Printable view
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List of potentially matching sequences

Send selected sequences to

Clustal W (multiple alignment)	▼	Submit Query
Select up to...		

☐ Include query sequence

Db	AC	Description
<input type="checkbox"/>	tr Q9RGF1	_CAMJE Alpha-2,3-sialyltransferase [cst-I] [Campylobact
<input type="checkbox"/>	tr Q32VR8	_CAMJE Alpha-2,3-sialyltransferase [cstI] [Campylobacte
<input type="checkbox"/>	tr Q5DT12	_CAMJE Putative alpha-2,3/-2,8 sialyltransferase [Campy
<input type="checkbox"/>	tr Q1KZ67	_CAMJE Alpha-2,3-sialyltransferase [cstII] [Campylobact
<input type="checkbox"/>	tr Q93MQ0	_CAMJE Alpha-2,3-/alpha-2,8-sialyltransferase [cstII] [
<input type="checkbox"/>	tr Q9F0M9	_CAMJE Alpha-2,3-sialyltransferase [cst-II] [Campylobac
<input type="checkbox"/>	tr Q9LAK3	_CAMJE Alpha-2,3/8-sialyltransferase (Alpha-2,3-/2,8-si
<input type="checkbox"/>	tr Q9L9Q5	_CAMJE Alpha-2,3-sialyltransferase (Sialyl transferase)
<input type="checkbox"/>	tr Q938X6	_CAMJE Alpha-2,3-/alpha-2,8-sialyltransferase [cstII] [
<input type="checkbox"/>	tr Q50FZ0	_CAMJE Cj81-011 (Fragment) [Campylobacter jejuni]

☐ tr Q93CZ5 _CAMJE Bifunctional alpha-2,3/-2,8-sialyltransferase [c
☐ tr Q0GH31 _CAMJE Alpha-2,3/8-sialyltransferase [cst-II] [Campylob
☐ tr Q0GH57 _CAMJE Alpha-2,3/8-sialyltransferase [cst-II] [Campylob
☐ tr Q0GH18 _CAMJE Alpha-2,3/8-sialyltransferase [cst-II] [Campylob
☐ tr Q93D05 _CAMJE Alpha-2,3-sialyltransferase [cst-II] [Campylobac
☐ tr Q1L2M7 _CAMJE Alpha-2,3/-2,8-sialyltransferase [cst-II] [Campy
☐ tr Q2TKA8 _CAMJE Putative alpha-2,3/8-sialyltransferase [Campylob
☐ tr Q7BP25 _CAMJE Hypothetical protein (Alpha-2,3 sialyltransferas
☐ tr Q32VQ2 _CAMJE Putative glycosyltransferase [Campylobacter jeju
☐ tr Q1W2L3 _HAEIN Lipopolysaccharide sialyltransferase [lic3B] [Ha
☐ tr Q4QM36 _HAEI8 CMP-neu5Ac--lipooligosaccharide alpha 2-3 sialyl
☐ tr Q32VR2 _CAMJE Putative glycosyltransferase [Campylobacter jeju
☐ tr Q5W602 _CAMJE Putative glycosyltransferase [Campylobacter jeju
☐ tr Q5M6Q2 _CAMJE Putative sugar transferase [HS23.17] [Campylobac
☐ tr Q6EF79 _CAMJE Putative glycosyltransferase [Campylobacter jeju
☐ tr Q9CLP3 _PASMU Hypothetical protein PM1174 [PM1174] [Pasteurell
☐ tr Q4QNI8 _HAEI8 CMP-Neu5Ac--lipooligosaccharide alpha 2-3 sialyl
☐ tr Q1W1W2 _HAEIN Lipopolysaccharide sialyltransferase [lic3A] [Ha
☐ tr Q6EF56 _CAMJE Putative glycosyltransferase [Campylobacter jeju
☐ tr Q5W603 _CAMJE Hypothetical protein [Campylobacter jejuni]
☐ tr Q29VV2 _CAMJE Putative glycosyl transferase [CJB1432c] [Campyl
☐ tr Q32VQ8 _CAMJE Hypothetical protein [Campylobacter jejuni subsp
☐ tr Q32VR3 _CAMJE Hypothetical protein [Campylobacter jejuni subsp
☐ tr Q32VQ3 _CAMJE Hypothetical protein [Campylobacter jejuni subsp
☐ tr Q0GH44 _CAMJE Alpha-2,3/8-sialyltransferase [cst-II] [Campylob
☐ tr Q5HT01 _CAMJR Capsular polysaccharide biosynthesis protein, pu
☐ tr Q5M6U5 _CAMJE Putative sugar transferase [HS41.06] [Campylobac
☐ tr Q6EBB5 _CAMJE Tgh007 (Fragment) [Campylobacter jejuni]
☐ tr Q17WF9 _HELAC Putative bifunctional alpha-2,3/-2,8-sialyltrans
☐ tr Q4HEK5 _CAMCO Alpha-2,3-sialyltransferase [CC01544] [Campyloba
☐ tr Q4HEL4 _CAMCO Alpha-2,3-sialyltransferase [CC01527] [Campyloba
☐ tr Q4HEJ9 _CAMCO Alpha-2,3-sialyltransferase [CC01538] [Campyloba
☐ tr Q17WF8 _HELAC Bifunctional alpha-2,3/-2,8-sialyltransferase [c
☐ sp P24324 Y352_HAEIN Hypothetical protein HI0352 (ORF1) [HI0352].
☐ tr Q5M6M2 _CAMJE Putative sugar transferase [HS19.11] [Campylobac
☐ tr Q5M6M5 _CAMJE Putative sugar transferase [HS19.08] [Campylobac
☐ tr Q5HT02 _CAMJR Capsular polysaccharide biosynthesis protein, pu
☐ tr Q4HR89 _CAMUP Hypothetical protein [CUP1274] [Campylobacter up
☐ tr Q4HEL1 _CAMCO DcbE, putative [CC01537] [Campylobacter coli RM2
☐ tr Q0P8I3 _CAMJE Capsular polysaccharide heptosyltransferase [hdd
☐ tr Q50FV9 _CAMJE Cj81-063 (Fragment) [Campylobacter jejuni]
☐ tr Q4HR98 _CAMUP Hypothetical protein [CUP1265] [Campylobacter up

☐ tr Q4HKU2 _CAMLA Glycosyl transferase family 8 family [CLA1010] [
☐ tr Q5M6U6 _CAMJE Putative sugar transferase [HS41.05] [Campylobac
☐ tr Q5M6S8 _CAMJE Putative sugar transferase [HS41.23] [Campylobac
☐ tr Q6EF57 _CAMJE Putative glycosyltransferase (Putative sugar tra
☐ tr Q29VV3 _CAMJE Putative glycosyl transferase [CJB1431c] [Campyl
☐ tr Q4HLH9 _CAMLA Hypothetical protein [CLA0678] [Campylobacter la
☐ tr Q4HR96 _CAMUP Glycosyl transferase, group 2 family protein [CU
☐ tr Q0P8J3 _CAMJE Putative sugar transferase [Cj1421c] [Campylobac
☐ tr Q0P8J2 _CAMJE Putative sugar transferase [Cj1422c] [Campylobac
☐ tr Q6EF89 _CAMJE Putative glycosyltransferase [Campylobacter jeju
☐ tr Q5M6M6 _CAMJE Putative sugar transferase [HS19.07] [Campylobac
☐ tr Q6EF76 _CAMJE Putative glycosyltransferase [Campylobacter jeju
☐ tr Q0P8I0 _CAMJE Putative sugar transferase [Cj1434c] [Campylobac
☐ tr Q4HR95 _CAMUP Glycosyl transferase, group 2 family protein, pu
☐ tr Q5M6P9 _CAMJE Putative sugar transferase (Cj81-080) [HS23.20]
☐ tr Q5M6R2 _CAMJE Putative sugar transferase [HS23.07] [Campylobac
☐ tr Q29VH2 _CAMJE Putative glycosyl transferase [Campylobacter jej
☐ tr Q29VW3 _CAMJE Putative sugar transferase [CJB1421c] [Campyloba
☐ tr Q4HRA0 _CAMUP Glycosyl transferase family 8 family [CUP1263] [
☐ tr Q4HSD1 _CAMUP Probable sugar transferase Cj1422c [CUP0322] [Ca
☐ tr Q4HQ44 _CAMUP Probable sugar transferase Cj1422c [CUP1233] [Ca
☐ tr Q4HLF9 _CAMLA Probable sugar transferase Cj1421c [CLA0655] [Ca
☐ tr Q4HLH0 _CAMLA Probable sugar transferase Cj1422c [CLA0667] [Ca
☐ tr Q4HNW9 _CAMUP Capsular polysaccharide biosynthesis protein, pu
☐ tr Q4HQ73 _CAMUP Capsular polysaccharide biosynthesis protein, pu
☐ tr Q0P8H6 _CAMJE Putative sugar transferase [Cj1438c] [Campylobac
☐ tr Q0P8I2 _CAMJE Putative sugar transferase [Cj1432c] [Campylobac
☐ tr Q4HTL3 _CAMUP Hypothetical protein [CUP0667] [Campylobacter up
☐ tr Q5M6N9 _CAMJE Putative sugar transferase [HS1.07] [Campylobact
☐ tr Q50FW8 _CAMJE Cj81-047 (Fragment) [Campylobacter jejuni]
☐ tr Q4HS04 _CAMUP Hypothetical protein [CUP1761] [Campylobacter up
☐ tr Q9CMP1 _PASMU HyaE (FcbE) [hyaE] [Pasteurella multocida]
☐ tr Q5M6S9 _CAMJE Putative sugar transferase [HS41.22] [Campylobac
☐ tr O85456 _PASMU HyaE [hyaE] [Pasteurella multocida]
☐ tr Q4HGT1 _CAMCO Bifunctional alpha-2,3/-2,8-sialyltransferase [C
☐ tr Q9AHN3 _PASMU DcbE [dcbE] [Pasteurella multocida]
☐ tr Q8L0V3 _ECOLI Hypothetical protein kfoB [kfoB] [Escherichia co.
☐ tr Q4HTC3 _CAMUP Capsular polysaccharide biosynthesis protein, pu
☐ tr Q6EBB2 _CAMJE Tgh012 (Fragment) [Campylobacter jejuni]
☐ tr Q6KCZ4 _ECOLI KfiB protein [kfiB] [Escherichia coli]
☐ tr Q43KB3 _9CHLB Similar to Chromosome segregation ATPases [Cpha2
☐ tr Q6EBB6 _CAMJE Tgh006 (Fragment) [Campylobacter jejuni]

- ☐ tr Q6EB08 _CAMJE Tgh120 (Fragment) [Campylobacter jejuni]
- ☐ tr Q7RS84 _PLAYO TERT (Fragment) [PY00479] [Plasmodium yoelii yoe]
- ☐ tr Q4Y918 _PLACH Hypothetical protein (Fragment) [PC000047.00.0]
- ☐ tr Q8IBW2 _PLAF7 Hypothetical protein MAL7P1.65 [MAL7P1.65] [Plas]
- ☐ tr Q9EMR1 _AMEPV AMV138 [AMV138] [Amsacta moorei entomopoxvirus (
- ☐ tr Q8I474 _PLAF7 Hypothetical protein PFE0130c [PFE0130c] [Plasmo

Graphical overview of the alignments

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to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs

(?) Help) (use ScanProsite for more details about PROSITE matches)

Profile hits

Pfam hits

CST-I



Alignments

tr Q9RGF1 Alpha-2,3-sialyltransferase [cst-I] [Campylobacter
Q9RGF1_CAMJE jejuni]

Score = 877 bits (2267), Expect = 0.0

Identities = 430/430 (100%), Positives = 430/430 (100%)

Query: 1 MTRTRMENELIVSKNMQNI IIIAGNGPSLKNIN YKRLPREYDVFR CNQFYFEDKY YL
MTRTRMENELIVSKNMQNI IIIAGNGPSLKNIN YKRLPREYDVFR CNQFYFEDKY YL
Sbjct: 1 MTRTRMENELIVSKNMQNI IIIAGNGPSLKNIN YKRLPREYDVFR CNQFYFEDKY YL

Query: 61 KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNL PFI ESND FLHQFY NFFPD
KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNL PFI ESND FLHQFY NFFPD
Sbjct: 61 KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNL PFI ESND FLHQFY NFFPD

Query: 121 YEVIENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI
YEVIENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI
Sbjct: 121 YEVIENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI

Query: 181 AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFP
AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFP
Sbjct: 181 AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFP

Query: 241 INNNFTLENKHNSINDILLTDNTPGV SFYKNQLKADNKIMLNFY NILH SKDNLIK
INNNFTLENKHNSINDILLTDNTPGV SFYKNQLKADNKIMLNFY NILH SKDNLIK
Sbjct: 241 INNNFTLENKHNSINDILLTDNTPGV SFYKNQLKADNKIMLNFY NILH SKDNLIK

Query: 301 EIAVLKKQTTQRAKARIQNHL SYKLGQALI INSKSVLGFLSLPFI ILSIVISHKQE
EIAVLKKQTTQRAKARIQNHL SYKLGQALI INSKSVLGFLSLPFI ILSIVISHKQE
Sbjct: 301 EIAVLKKQTTQRAKARIQNHL SYKLGQALI INSKSVLGFLSLPFI ILSIVISHKQE

Query: 361 KFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGE EFIKAGKNWYGE GYIKFIF
KFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGE EFIKAGKNWYGE GYIKFIF
Sbjct: 361 KFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGE EFIKAGKNWYGE GYIKFIF

Query: 421 RLKREFEKGE 430
RLKREFEKGE
Sbjct: 421 RLKREFEKGE 430

tr Q32VR8 Alpha-2,3-sialyltransferase [cstI] [Campylobacter
Q32VR8_CAMJE jejuni subsp.
jejuni]

Score = 875 bits (2261), Expect = 0.0

Identities = 429/430 (99%), Positives = 429/430 (99%)

Query: 1 MTRTRMENELIVSKNMQNI IIIAGNGPSLKNIN YKRLPREYDVFR CNQFYFEDKY YL
MTRTRMENELIVSKNMQNI IIIAGNGPSLKNIN YKRLPREYDVFR CNQFYFEDKY YL
Sbjct: 1 MTRTRMENELIVSKNMQNI IIIAGNGPSLKNIN YKRLPREYDVFR CNQFYFEDKY YL

Query: 61 KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNL PFIESNDFLHQFY NFFPD
KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNL PFIESNDFLHQFY NFFPD
Sbjct: 61 KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNL PFIESNDFLHQFY NFFPD

Query: 121 YEV IENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI
YEV IENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI
Sbjct: 121 YEV IENLKEFYAYIKYNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVI

Query: 181 AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFP
AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFP
Sbjct: 181 AMSTNIKTIFPGIKDFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFP

Query: 241 INNFTLENKHNN SINDILLTDNTPGV SFYKNQLKADNKIMLNFYNI LHSKDNL IK
INNFTLENKHNN SINDILLTDNTPGV SFYKNQLKADNKIMLNFYNI LHSKD NL IK
Sbjct: 241 INNFTLENKHNN SINDILLTDNTPGV SFYKNQLKADNKIMLNFYNI LHSKD TLI K

Query: 301 EIAVLKKQTTQRAKARIQNHL SYKLGQALI INSKSVLGFLSLPFIILSIVISHKQE
EIAVLKKQTTQRAKARIQNHL SYKLGQALI INSKSVLGFLSLPFIILSIVISHKQE
Sbjct: 301 EIAVLKKQTTQRAKARIQNHL SYKLGQALI INSKSVLGFLSLPFIILSIVISHKQE

Query: 361 KFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGE EFIKAGKNWYGE GYIKFIF
KFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGE EFIKAGKNWYGE GYIKFIF
Sbjct: 361 KFKVKKNPNLALPPLETYPDYNEALKEKECFTYKLGE EFIKAGKNWYGE GYIKFIF

Query: 421 RLKREFEKGE 430
RLKREFEKGE
Sbjct: 421 RLKREFEKGE 430

tr Q5DT12 Putative alpha-2,3/-2,8 sialyltransferase
Q5DT12_CAMJE [Campylobacter jejuni]

Score = 301 bits (770), Expect = 4e-80

Identities = 147/274 (53%), Positives = 189/274 (68%), Gaps = 7/27

Query: 16 MQNI IIIAGNGPSLKNIN YKRLPREYDVFR CNQFYFEDKY YLGKKI KAVFFNPGVFL
M+ +IIAGNGPSLK I+Y RLP ++DVFR CNQFYFEDKY YLGKK KAVF+NP +F
Sbjct: 1 MKKVIIAGNGPSLKEIDYSRLPNDFDVFR CNQFYFEDKY YLGKKCKAVFY NPSLFF

Query: 76 TAKQLILKNEYEIKNIFCSTFNL PFIESNDFLHQFY NFFPD AKLGYEV IENLKEFY

Sbjct: 61 T K LI EYE + I CS FNL IES +FL FY++FPDA LGY+ + LKEF
TLKHLIQNQEYETELIVCSNFNLT HIESENFLKNFYDYFPDAHLGYDFFKQLKEFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP
++EIYFN+RITSG+YMCA+AIALGYK IYL GIDFY+ Y F+ N+ +

Sbjct: 121 FHEIYFNQRITSGIYMCVAIAIALGYKEIYLSGIDFYQNGSSYAFDTKQKNLLKL--

Query: 196 FKPSNC----HSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTL
FK N HSK D++AL+ L+ YK+ +Y LC +S+LAN L+ N+N+NF +

Sbjct: 178 FKNDNSHYIGHSKNTDLKALEFLEKTYKIKLYCLCPNSLLANFIELAPNLNSNFII

Query: 252 NNSINDILLTDNTPGVSFYKNQLKADNKIMLNFY 285
NN DIL+ + F KN + KI N Y

Sbjct: 238 NNYTKDILIPSSEAYGKFSKNIIFKKIKIKENIY 271

tr Q1KZ67 Alpha-2,3-sialyltransferase [cstII] [Campylobacter
Q1KZ67_CAMJE jejuni]

Score = 291 bits (744), Expect = 5e-77

Identities = 145/272 (53%), Positives = 189/272 (69%), Gaps = 3/27

Query: 16 MQNIIIIAGNGPSLKNINYKRLPREYDVFR CNQFYFEDKYYLGKKIKAVFFNPGVFL
M+ +IIAGNGPSLK I+Y RLP ++DVFR CNQFYFEDKYYLGKK KAVF+N +F

Sbjct: 1 MKKVIIAGNGPSLKEIDYSRLPNDFDVFR CNQFYFEDKYYLGKKCKAVFYNTILFF

Query: 76 TAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDAKLGYEV IENLKEFY
T K LI EYE + I CS FNL IE+ +FL FY++FPDA+LGY+ + LKEF

Sbjct: 61 TLKHLIQNQEYETELIMCSNFNLAHIENENFLKNFYDYFPDARLGYDFFKQLKEFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP
++EIYFN+RITSGVYMCA+AIALGYK IYL GIDFY+ Y F+ N+ + P

Sbjct: 121 FHEIYFNQRITSGVYMCAVAIAIALGYKEIYLTGIDFYDNGGGYAFDTKKENLLKLAP

Query: 196 FKPSNC-HSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENK
+ HSK D++AL+ L+ Y++ +Y LC +S+LAN L+ N+N+NF ++ K

Sbjct: 181 DRSHYIGHSKNTDLKALEFLEKTYEIKLYCLCPNSLLANFIELAPNLNSNFIIQEK

Query: 255 INDILLTDNTPGVSFYKN-QLKADNKIMLNFY 285
I DIL+ +F KN L K+ N Y

Sbjct: 240 IKDILIPSKEAYNNFSKNFNLPNPKPKLENIY 271

tr Q93MQ0 Alpha-2,3-/alpha-2,8-sialyltransferase [cstII]
Q93MQ0_CAMJE [Campylobacter]

jejuni]

Score = 290 bits (742), Expect = 8e-77

Identities = 142/271 (52%), Positives = 186/271 (68%), Gaps = 2/27

Query: 16 MQNIIIAGNGPSLKNINYKRLPREYDVFRGNQFYFEDKYYLGKKIKAVFFNPGVFL
M+ +II+GNGPSLK I+Y RLP ++DVFRGNQFYFEDKYYLGKK KAVF+NPG+F
Sbjct: 1 MKKVIIISGNGPSLKEIDYSRLPNDFDVFRGNQFYFEDKYYLGKKFKAVFYNPGLFF

Query: 76 TAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFFPDALGYEVIENTLKEFY
T K LI EYE + I CS +N +E+ +F+ FY++FPDA LGY+ + LKEF
Sbjct: 61 TLKHLIQNQEYETELIMCSNYNQAHLNENFVKTFYDYFPDAHLGYDFFKQLKEFN

Query: 136 YNEIYFNKRITSGVYMCAIAIALGYKTIYLCGIDFYEGDVIYPFEAMSTNIKTIFP
++EIIY N+RITSGVYMCA+AIALGYK IYL GIDFY+ Y F+ N+ + P
Sbjct: 121 FHEIYLNQRITSGVYMCAVAIALGYKEIYLSGIDFYQNGSSYAFDTKQENLLKLAP

Query: 196 FKPSNC-HSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLSININNNFTLENK
+ HSK DI+AL+ L+ YK+ +Y LC +S+LAN L+ N+N+NF ++ K
Sbjct: 181 DRSHYIGHSKNTDIKALEFLEKTYKIKLYCLCPNSLLANFIELAPNLNSNFIIQEK

Query: 255 INDILLTDNTPGVSFYKNQLKADNKIMLNFY 285
DIL+ + F KN KI N Y
Sbjct: 240 TKDILIPSSEAYGKFSKNINFKKIKIKENIY 270

Description of Disclosure:

[1020] An example of a sialyltransferase that is useful in the claimed methods is CST-I from Campylobacter (see, for example, U.S. Pat. Nos. 6,503,744, 6,096,529, and 6,210,933 and WO99/49051, and published U.S. Pat. Application 2002/2,042,369). This enzyme catalyzes the transfer of sialic acid to the Gal of a Gal.beta.1,4Glc or Gal.beta.1,3GalNAc. Other exemplary sialyltransferases of use in the present invention include those isolated from Campylobacter jejuni, including the .alpha.(2,3) sialyltransferase. See, e.g, WO99/49051.